

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/507,156  
Source: PG 10  
Date Processed by STIC: 11/21/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK-SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/507,156

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos        was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will  
                               prevent "wrapping."
  
- 2      Invalid Line Length    The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino        The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers;  
     Numbering                use **space characters**, instead.
  
- 4      Non-ASCII                The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please  
                                     ensure your subsequent submission is saved in **ASCII text**.
  
- 5      Variable Length        Sequence(s)          contain n's or Xaa's representing more than one residue. **Per Sequence Rules,**  
                                     each n or Xaa can only represent a single residue. Please present the **maximum** number of each  
                                     residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0            A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"                      sequences(s)         . Normally, PatentIn would automatically generate this section from the  
                                     previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
                                     the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for**  
                                     **Artificial or Unknown sequences.**
  
- 7      Skipped Sequences      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
     (OLD RULES)                (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                     (i)        SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                     This sequence is intentionally skipped  
  
                                     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8      Skipped Sequences      Sequence(s)          missing. If **intentional**, please insert the following lines for each skipped sequence.  
     (NEW RULES)                <210> sequence id number  
                                     <400> sequence id number  
                                     000
  
- 9      Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)                Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                                     In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10     Invalid <213>            Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or  
     Response                    scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or  
                                     is Artificial Sequence
  
- 11     Use of <220>            Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
     →                            Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or  
                                     "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12     PatentIn 2.0            Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"                        resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                                     listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13     Misuse of n/Xaa        "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



PCT

## RAW SEQUENCE LISTING

DATE: 11/21/2005

PATENT APPLICATION: US/10/507,156

TIME: 15:43:04

Input Set : A:\N0008001.app

Output Set: N:\CRF4\11212005\J507156.raw

3 <110> APPLICANT: OKU, TADATAKE  
 4 NISHIO, TOSHIYUKI  
 5 KAWACHI, RYU  
 6 SURUGA, KOHEI  
 8 <120> TITLE OF INVENTION: NOVEL HEME PEPTIDE  
 10 <130> FILE REFERENCE: N0008.0001  
 12 <140> CURRENT APPLICATION NUMBER: 10/507,156  
 13 <141> CURRENT FILING DATE: 2004-09-07  
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP03/02394  
 16 <151> PRIOR FILING DATE: 2003-02-28  
 18 <150> PRIOR APPLICATION NUMBER: JP 2002-058086  
 19 <151> PRIOR FILING DATE: 2002-03-04  
 21 <160> NUMBER OF SEQ ID NOS: 18  
 23 <170> SOFTWARE: PatentIn Ver. 3.2

Does Not Comply  
Corrected Diskette Needed

## ERRORED SEQUENCES

335 <210> SEQ ID NO: 14  
 336 <211> LENGTH: 18 4 shown below  
 337 <212> TYPE: PRT  
 338 <213> ORGANISM: Artificial Sequence  
 340 <220> FEATURE:  
 341 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 342 peptide  
 344 <400> SEQUENCE: 14  
 E--> 345 Thr Val Glu Lys

( see p.2 )

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2

<210> 11  
<211> 75  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Formula  
peptide

<220>

<221> MISC\_FEATURE

<222> (1)..(20)

<223> this region may encompass a hydrogen atom or 1-20 variable amino acids

<220>

<221> MISC\_FEATURE

<222> (22)..(23)

<223> any amino acid

<220>

<221> MISC\_FEATURE

<222> (25)

<223> His, Lys or Arg

<220>

<221> MISC\_FEATURE

<222> (26)..(75)

<223> this region may encompass a hydroxyl group or 1-50 variable amino acids

<220>

<223> see specification as filed for detailed description of preferred embodiments

<400> 11

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1 5 10 15

Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
65 70 75

insufficient explanation  
(give source of genetic material - see item 11 on Error

↓  
Xaa can only represent a single amino acid, nothing else. This error appears in subsequent sequences.  
OK

summary sheet)

This error appears

in subsequent sequences

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/507,156

DATE: 11/21/2005

TIME: 15:43:05

Input Set : A:\N0008001.app

Output Set: N:\CRF4\11212005\J507156.raw

L:220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0  
L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:16  
L:226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:32  
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:48  
L:232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:64  
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0  
L:275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:16  
L:278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:32  
L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:48  
L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:64  
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0  
L:322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:16  
L:325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:32  
L:328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:48  
L:331 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:64  
L:345 M:252 E: No. of Seq. differs, <211> LENGTH:Input:18 Found:4 SEQ:14